

&lt;110&gt; Arkray, Inc.

&lt;120&gt; Method for producing glucose dehydrogenase

&lt;130&gt; G843-OPC4051

&lt;150&gt; JP 2003-82739

&lt;151&gt; 2003-03-25

&lt;160&gt; 15

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 2467

&lt;212&gt; DNA

&lt;213&gt; Burkholderia cepacia

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (258)..(761)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (764)..(2380)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2386)..(2466)

&lt;400&gt; 1

```

aagctttctg ttigtattgca cgcgattcta accgagcgtc tgtgaggcgg aacgcgacat 60
gcttcgtgtc gcacacgtgt cgcgccgacg acacaaaaat gcagcgaaat ggctgatcgt 120
tacgaatggc tgacacattg aatggactat aaaaccattg tccgttccgg aatgtgcgcg 180
tacatttcag gtccgcgcgg atttttigaga aatatcaagc gtggttttcc cgaatccggt 240
gttcgagaga aggaaac atg cac aac gac aac act ccc cac tgc cgt cgc      290

```

Met His Asn Asp Asn Thr Pro His Ser Arg Arg

1

5

10

```

cac ggc gac gca gcc gca tca ggc atc acg cgg cgt caa tgg ttg caa      338
His Gly Asp Ala Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln

```

15

20

25

ggc gcg ctg gcg ctg acc gca gcg ggc ctc acg ggt tgc ctg aca ttg	386
Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu	
30 35 40	
cgg gcg ctt gca gac aac ccc ggc act gcg ccg ctc gat acg ttc atg	434
Arg Ala Leu Ala Asp Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met	
45 50 55	
acg ctt tcc gaa tgc ctg acc ggc aag aaa ggg ctc agc cgc gtg atc	482
Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile	
60 65 70 75	
ggc gag cgc ctg ctg cag gcg ctg cag aag ggc tgc ttc aag acg gcc	530
Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala	
80 85 90	
gac agc ctg ccg cag ctc gcc ggc gcg ctc gcg tcc ggt tgc ctg acg	578
Asp Ser Leu Pro Gln Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr	
95 100 105	
cct gaa cag gaa tgc ctc gca ctg acg atc ctc gag gcc tgg tat ctc	626
Pro Glu Gln Glu Ser Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu	
110 115 120	
ggc atc gtc gac aac gtc gtg att acg tac gag gaa gca tta atg ttc	674
Gly Ile Val Asp Asn Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe	
125 130 135	
ggc gtc gtg tcc gat acg ctc gtg atc cgt tgc tat tgc ccc aac aaa	722
Gly Val Val Ser Asp Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys	
140 145 150 155	
ccc ggc ttc tgg gcc gac aaa ccg atc gag agg caa gcc tg atg gcc	769
Pro Gly Phe Trp Ala Asp Lys Pro Ile Glu Arg Gln Ala Met Ala	
160 165 170	
gat acc gat acg caa aag gcc gac gtc gtc gtc gtt gga tgc ggt gtc	817
Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser Gly Val	
175 180 185	
gcg ggc gcg atc gtc gcg cat cag ctc gcg atg gcg ggc aag gcg gtg	865
Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys Ala Val	
190 195 200	
atc ctg ctc gaa gcg ggc ccg cgc atg ccg cgc tgg gaa atc gtc gag	913
Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile Val Glu	
205 210 215	
cgc ttc cgc aat cag ccc gac aag atg gac ttc atg gcg ccg tac ccg	961
Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro Tyr Pro	
220 225 230	
tgc agc ccc tgg gcg ccg cat ccc gag tac ggc ccg ccg aac gac tac	1009
Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn Asp Tyr	
235 240 245 250	
ctg atc ctg aag ggc gag cac aag ttc aac tgc cag tac atc cgc gcg	1057

Leu	Ile	Leu	Lys	Gly	Glu	His	Lys	Phe	Asn	Ser	Gln	Tyr	Ile	Arg	Ala	
				255					260					265		
gtg	ggc	ggc	acg	acg	tgg	cac	tgg	gcc	gcg	tcg	gcg	tgg	cgc	ttc	att	1105
Val	Gly	Gly	Thr	Thr	Trp	His	Trp	Ala	Ala	Ser	Ala	Trp	Arg	Phe	Ile	
			270					275					280			
ccg	aac	gac	ttc	aag	atg	aag	agc	gtg	tac	ggc	gtc	ggc	cgc	gac	tgg	1153
Pro	Asn	Asp	Phe	Lys	Met	Lys	Ser	Val	Tyr	Gly	Val	Gly	Arg	Asp	Trp	
		285					290					295				
ccg	atc	cag	tac	gac	gat	ctc	gag	ccg	tac	tat	cag	cgc	gcg	gag	gaa	1201
Pro	Ile	Gln	Tyr	Asp	Asp	Leu	Glu	Pro	Tyr	Tyr	Gln	Arg	Ala	Glu	Glu	
	300					305					310					
gag	ctc	ggc	gtg	tgg	ggc	ccg	ggc	ccc	gag	gaa	gat	ctg	tac	tcg	ccg	1249
Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr	Ser	Pro	
315					320					325					330	
cgc	aag	cag	ccg	tat	ccg	atg	ccg	ccg	ctg	ccg	ttg	tcg	ttc	aac	gag	1297
Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe	Asn	Glu	
			335					340						345		
cag	acc	atc	aag	acg	gcg	ctg	aac	aac	tac	gat	ccg	aag	ttc	cat	gtc	1345
Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe	His	Val	
			350					355					360			
gtg	acc	gag	ccg	gtc	gcg	cgc	aac	agc	cgc	ccg	tac	gac	ggc	cgc	ccg	1393
Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly	Arg	Pro	
		365					370					375				
act	tgt	tgc	ggc	aac	aac	aac	tgc	atg	ccg	atc	tgc	ccg	atc	ggc	gcg	1441
Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile	Gly	Ala	
	380					385					390					
atg	tac	aac	ggc	atc	gtg	cac	gtc	gag	aag	gcc	gaa	cgc	gcc	ggc	gcg	1489
Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala	Gly	Ala	
395					400					405					410	
aag	ctg	atc	gag	aac	gcg	gtc	gtc	tac	aag	ctc	gag	acg	ggc	ccg	gac	1537
Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly	Pro	Asp	
			415					420					425			
aag	cgc	atc	gtc	gcg	gcg	ctc	tac	aag	gac	aag	acg	ggc	gcc	gag	cat	1585
Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala	Glu	His	
			430					435					440			
cgc	gtc	gaa	ggc	aag	tat	ttc	gtg	ctc	gcc	gcg	aac	ggc	atc	gag	acg	1633
Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile	Glu	Thr	
		445					450					455				
ccg	aag	atc	ctg	ctg	atg	tcc	gcg	aac	cgc	gat	ttc	ccg	aac	ggt	gtc	1681
Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn	Gly	Val	
	460					465					470					
gcg	aac	agc	tcg	gac	atg	gtc	ggc	cgc	aac	ctg	atg	gac	cat	ccg	ggc	1729
Ala	Asn	Ser	Ser	Asp	Met	Val	Gly	Arg	Asn	Leu	Met	Asp	His	Pro	Gly	

475		480		485		490	
acc ggc gtg tgc ttc tat gcg agc gag aag ctg tgg ccg ggc cgc ggc	1777						
Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly							
		495		500		505	
ccg cag gag atg acg tgc ctg atc ggt ttc cgc gac ggt ccg ttc cgc	1825						
Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro Phe Arg							
		510		515		520	
gcg acc gaa gcg gcg aag aag atc cac ctg tgc aac ctg tgc cgc atc	1873						
Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser Arg Ile							
		525		530		535	
gac cag gag acg cag aag atc ttc aag gcc ggc aag ctg atg aag ccc	1921						
Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met Lys Pro							
		540		545		550	
gac gag ctc gac gcg cag atc cgc gac cgt tcc gca cgc tac gtg cag	1969						
Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr Val Gln							
		555		560		565	
ttc gac tgc ttc cac gaa atc ctg ccg caa ccc gag aac cgc atc gtg	2017						
Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val							
		575		580		585	
ccg agc aag acg gcg acc gat gcg atc ggc att ccg cgc ccc gag atc	2065						
Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro Glu Ile							
		590		595		600	
acg tat gcg atc gac gac tac gtg aag cgc ggc gcc gcg cat acg cgc	2113						
Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg							
		605		610		615	
gag gtc tac gcg acc gcc gcg aag gtg ctc ggc ggc acg gac gtc gtg	2161						
Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp Val Val							
		620		625		630	
ttc aac gac gaa ttc gcg ccg aac aat cac atc acg ggc tgc acg atc	2209						
Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser Thr Ile							
		635		640		645	
atg ggc gcc gat gcg cgc gac tcc gtc gtc gac aag gac tgc cgc acg	2257						
Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys Arg Thr							
		655		660		665	
ttc gac cat ccg aac ctg ttc att tgc agc agc gcg acg atg ccg acc	2305						
Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met Pro Thr							
		670		675		680	
gtc ggt acc gta aac gtg acg ctg acg atc gcc gcg ctc gcg ctg cgg	2353						
Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg							
		685		690		695	
atg tgc gac acg ctg aag aag gaa gtc tgacc gtg cgg aaa tct act ctc	2403						
Met Ser Asp Thr Leu Lys Lys Glu Val Val Arg Lys Ser Thr Leu							
		700		705		710	

act ttc ctc atc gcc ggc tgc ctc gcg ttc ccg ggc ttc gcg cgc gcg 2451  
 Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe Ala Arg Ala  
       715                      720                      725

gcc gat gcg gcc gat c 2467  
 Ala Asp Ala Ala Asp  
 730

<210> 2

<211> 168

<212> PRT

<213> Burkholderia cepacia

<400> 2

Met His Asn Asp Asn Thr Pro His Ser Arg Arg His Gly Asp Ala Ala  
   1                      5                      10                      15  
 Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln Gly Ala Leu Ala Leu  
                       20                      25                      30  
 Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu Arg Ala Leu Ala Asp  
                       35                      40                      45  
 Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser  
                       50                      55                      60  
 Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu  
   65                      70                      75                      80  
 Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln  
                       85                      90                      95  
 Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser  
                       100                      105                      110  
 Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn  
                       115                      120                      125  
 Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp  
                       130                      135                      140  
 Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys Pro Gly Phe Trp Ala  
   145                      150                      155                      160  
 Asp Lys Pro Ile Glu Arg Gln Ala  
                       165

<210> 3

<211> 539

<212> PRT

<213> Burkholderia cepacia

<400> 3

Met Ala Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser  
   1                      5                      10                      15

Gly	Val	Ala	Gly	Ala	Ile	Val	Ala	His	Gln	Leu	Ala	Met	Ala	Gly	Lys	20	25	30
Ala	Val	Ile	Leu	Leu	Glu	Ala	Gly	Pro	Arg	Met	Pro	Arg	Trp	Glu	Ile	35	40	45
Val	Glu	Arg	Phe	Arg	Asn	Gln	Pro	Asp	Lys	Met	Asp	Phe	Met	Ala	Pro	50	55	60
Tyr	Pro	Ser	Ser	Pro	Trp	Ala	Pro	His	Pro	Glu	Tyr	Gly	Pro	Pro	Asn	65	70	75
Asp	Tyr	Leu	Ile	Leu	Lys	Gly	Glu	His	Lys	Phe	Asn	Ser	Gln	Tyr	Ile	85	90	95
Arg	Ala	Val	Gly	Gly	Thr	Thr	Trp	His	Trp	Ala	Ala	Ser	Ala	Trp	Arg	100	105	110
Phe	Ile	Pro	Asn	Asp	Phe	Lys	Met	Lys	Ser	Val	Tyr	Gly	Val	Gly	Arg	115	120	125
Asp	Trp	Pro	Ile	Gln	Tyr	Asp	Asp	Leu	Glu	Pro	Tyr	Tyr	Gln	Arg	Ala	130	135	140
Glu	Glu	Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr	145	150	155
Ser	Pro	Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe	165	170	175
Asn	Glu	Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe	180	185	190
His	Val	Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly	195	200	205
Arg	Pro	Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile	210	215	220
Gly	Ala	Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala	225	230	235
Gly	Ala	Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly	245	250	255
Pro	Asp	Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala	260	265	270
Glu	His	Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile	275	280	285
Glu	Thr	Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn	290	295	300
Gly	Val	Ala	Asn	Ser	Ser	Asp	Met	Val	Gly	Arg	Asn	Leu	Met	Asp	His	305	310	315
Pro	Gly	Thr	Gly	Val	Ser	Phe	Tyr	Ala	Ser	Glu	Lys	Leu	Trp	Pro	Gly	325	330	335
Arg	Gly	Pro	Gln	Glu	Met	Thr	Ser	Leu	Ile	Gly	Phe	Arg	Asp	Gly	Pro	340	345	350
Phe	Arg	Ala	Thr	Glu	Ala	Ala	Lys	Lys	Ile	His	Leu	Ser	Asn	Leu	Ser			

355						360						365					
Arg	Ile	Asp	Gln	Glu	Thr	Gln	Lys	Ile	Phe	Lys	Ala	Gly	Lys	Leu	Met		
370						375						380					
Lys	Pro	Asp	Glu	Leu	Asp	Ala	Gln	Ile	Arg	Asp	Arg	Ser	Ala	Arg	Tyr		
385						390						395					
Val	Gln	Phe	Asp	Cys	Phe	His	Glu	Ile	Leu	Pro	Gln	Pro	Glu	Asn	Arg		
405						410						415					
Ile	Val	Pro	Ser	Lys	Thr	Ala	Thr	Asp	Ala	Ile	Gly	Ile	Pro	Arg	Pro		
420						425						430					
Glu	Ile	Thr	Tyr	Ala	Ile	Asp	Asp	Tyr	Val	Lys	Arg	Gly	Ala	Ala	His		
435						440						445					
Thr	Arg	Glu	Val	Tyr	Ala	Thr	Ala	Ala	Lys	Val	Leu	Gly	Gly	Thr	Asp		
450						455						460					
Val	Val	Phe	Asn	Asp	Glu	Phe	Ala	Pro	Asn	Asn	His	Ile	Thr	Gly	Ser		
465						470						475					
Thr	Ile	Met	Gly	Ala	Asp	Ala	Arg	Asp	Ser	Val	Val	Asp	Lys	Asp	Cys		
485						490						495					
Arg	Thr	Phe	Asp	His	Pro	Asn	Leu	Phe	Ile	Ser	Ser	Ser	Ala	Thr	Met		
500						505						510					
Pro	Thr	Val	Gly	Thr	Val	Asn	Val	Thr	Leu	Thr	Ile	Ala	Ala	Leu	Ala		
515						520						525					
Leu	Arg	Met	Ser	Asp	Thr	Leu	Lys	Lys	Glu	Val							
530						535											

$\langle 210 \rangle$  4  
 $\langle 211 \rangle$  27  
 $\langle 212 \rangle$  PRT  
 $\langle 213 \rangle$  Burkholderia cepacia

<400> 4  
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu  
1 5 10 15  
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp  
20 25

$\langle 210 \rangle$  5  
 $\langle 211 \rangle$  16  
 $\langle 212 \rangle$  PRT  
 $\langle 213 \rangle$  Burkholderia cepacia

<400> 5  
Ala Asp Ala Ala Asp Pro Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala  
1 5 10 15

<210> 6  
 <211> 25  
 <212> PRT  
 <213> Artificial Sequence.

<220>  
 <223> Description of Artificial Sequence:consensus

<220>  
 <221> UNSURE  
 <222> (6, 17, 18, 19, 22)  
 <223> Xaa=unknown

<400> 6  
 Ala Asp Ala Ala Asp Xaa Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala  
           1                  5                  10                  15  
 Xaa Xaa Xaa Asp Cys Xaa Ala Cys His  
                   20                  25

<210> 7  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 7  
 tgcaccgtgc ggaaatctac tctcact 27

<210> 8  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 8  
 acttccttct tcagcgtgtc cgacatc 27

<210> 9



&lt;211&gt; 1441

&lt;212&gt; DNA

&lt;213&gt; Burkholderia cepacia

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (121)..(1398)

&lt;400&gt; 9

```

tccgaacctg ttcatctcga gcagcgcgac gatgccgacc gtcggtaccg taaacgtgac 60
gcctgacgac gccgcgctcg cgctgcggat gtcggacacg ctgaagaagg aagcttgacc 120
gtg cgg aaa tct act ctc act ttc ctc atc gcc ggc tgc ctc gcg ttg 168
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
      1              5              10              15
ccg ggc ttc gcg cgc gcg gcc gat gcg gcc gat ccg gcg ctg gtc aag 216
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
              20              25              30
cgc ggc gaa tac ctc gcg acc gcc atg ccg gta ccg atg ctc ggc aag 264
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
              35              40              45
atc tac acg agc aac atc acg ccc gat ccc gat acg ggc gac tgc atg 312
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
              50              55              60
gcc tgc cac acc gtg aag ggc ggc aag ccg tac gcg ggc ggc ctt ggc 360
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
      65              70              75              80
ggc atc ggc aaa tgg acg ttc gag gac ttc gag cgc gcg gtg cgg cac 408
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
              85              90              95
ggc gtg tcg aag aac ggc gac aac ctg tat ccg gcg atg ccg tac gtg 456
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
              100              105              110
tcg tac gcg aag atc aag gac gac gac gta cgc gcg ctg tac gcc tac 504
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr
              115              120              125
ttc atg cac ggc gtc gag ccg gtc aag cag gcg ccg ccg aag aac gag 552
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
              130              135              140
atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg 600
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp
      145              150              155              160
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc gcc 648
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala

```

				165				170				175					
gaa	tgg	aat	cgc	ggc	gcg	tat	ctg	gtg	cag	ggt	ctc	gcg	cac	tgc	agc	696	
Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	His	Cys	Ser		
180				185				190									
acg	tgc	cac	acg	ccg	cgc	ggc	atc	gcg	atg	cag	gag	aag	tgc	ctc	gac	744	
Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp		
195				200				205									
gaa	acc	ggc	ggc	agc	ttc	ctc	gcg	ggg	tgc	gtg	ctc	gcc	ggc	tgg	gac	792	
Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ala	Gly	Ser	Val	Leu	Ala	Gly	Trp	Asp		
210				215				220									
ggc	tac	aac	atc	acg	tgc	gac	ccg	aat	gcg	ggg	atc	ggc	agc	tgg	acg	840	
Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Ser	Trp	Thr		
225				230				235				240					
cag	cag	cag	ctc	gtg	cag	tat	tig	cgc	acc	ggc	agc	gtg	ccg	ggc	gtc	888	
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Val		
245				250				255									
gcg	cag	gcg	gcc	ggg	ccg	atg	gcc	gag	gcg	gtc	gag	cac	agc	ttc	tgc	936	
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Val	Glu	His	Ser	Phe	Ser		
260				265				270									
aag	atg	acc	gaa	gcg	gac	atc	ggt	gcg	atc	gcc	acg	tac	gtc	cgc	acg	984	
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr		
275				280				285									
gtg	ccg	gcc	gtt	gcc	gac	agc	aac	gcg	aag	cag	ccg	cgg	tgc	tgc	tgg	1032	
Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp		
290				295				300									
ggc	aag	ccg	gcc	gag	gac	ggg	ctg	aag	ctg	cgc	ggt	gtc	gcg	ctc	gcg	1080	
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala		
305				310				315				320					
tgc	tgc	ggc	atc	gat	ccg	gcg	cgg	ctg	tat	ctc	ggc	aac	tgc	gcg	acg	1128	
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr		
325				330				335									
tgc	cac	cag	atg	cag	ggc	aag	ggc	acg	ccg	gac	ggc	tat	tac	ccg	tgc	1176	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser		
340				345				350									
ctg	ttc	cac	aac	tcc	acc	gtc	ggc	gcg	tgc	aat	ccg	tgc	aac	ctc	gtg	1224	
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Ser	Asn	Leu	Val		
355				360				365									
cag	gtg	atc	ctg	aac	ggc	gtg	cag	cgc	aag	atc	ggc	agc	gag	gat	atc	1272	
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile		
370				375				380									
ggg	atg	ccc	gct	ttc	cgc	tac	gat	ctg	aac	gac	gcg	cag	atc	gcc	gcg	1320	
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala		
385				390				395				400					

ctg acg aac tac gtg acc gcg cag ttc ggc aat ccg gcg gcg aag gtg 1368  
 Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val  
 405 410 415  
 acg gag cag gac gtc gcg aag ctg cgc tga catagtcggg cgcgccgaca 1418  
 Thr Glu Gln Asp Val Ala Lys Leu Arg  
 420 425  
 cggcgcgaacc gataggacag gag 1441

<210> 10

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 10

Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu  
 1 5 10 15  
 Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys  
 20 25 30  
 Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys  
 35 40 45  
 Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met  
 50 55 60  
 Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly  
 65 70 75 80  
 Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His  
 85 90 95  
 Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val  
 100 105 110  
 Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr  
 115 120 125  
 Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu  
 130 135 140  
 Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp  
 145 150 155 160  
 Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala  
 165 170 175  
 Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser  
 180 185 190  
 Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp  
 195 200 205  
 Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp  
 210 215 220  
 Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr

12/13

225		230		235		240									
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Val
		245							250					255	
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Val	Glu	His	Ser	Phe	Ser
		260							265					270	
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr
		275						280					285		
Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp
	290						295				300				
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
305					310					315				320	
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
			325						330					335	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser
		340						345					350		
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Ser	Asn	Leu	Val
	355						360					365			
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile
	370					375					380				
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala
385					390					395				400	
Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val
			405						410				415		
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg							
		420						425							

<210> 11

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: heme binding motif

<220>

<221> UNSURE

<222> (2, 3)

<223> Xaa=unknown

<400> 11

Cys Xaa Xaa Cys His

1

5

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

catgccatgg cacacaacga caacac

26

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

gtcgacgatc ttcttccagc cgaacatcac

30

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

tggccatggt tgaagccaga gagttacttt

30

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15

ttatttactc tcctgcggcg acaaattgtg

30